

2nd Substitute Specification – Clean Version

SEQUENCE LISTING

<110> THE UNIVERSITY OF QUEENSLAND

<120> A NOVEL PLANT PROMOTER AND USES THEREFOR

<130> 2209376/EJH

<140>

<141>

<150> PP5572

<151> 1998

-08-31

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

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<221> CDS

<222> (88)..(1539)

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Met Gly Phe Lys Ala Met Asp Gln Thr
1 5

ccc ttg ttg tcc aag atg gct att ggg gat gga cat ggc gaa tca tcc 162
Pro Leu Leu Ser Lys Met Ala Ile Gly Asp Gly His Gly Glu Ser Ser
10 15 20 25

cca tac ttt gat gga tgg aag gct tat gat caa aac ccc ttt cat ccc 210
Pro Tyr Phe Asp Gly Trp Lys Ala Tyr Asp Gln Asn Pro Phe His Pro
30 35 40

aca gat aat cct aac ggt gtt atg caa atg ggt ctt gct gag aat cag 258
Thr Asp Asn Pro Asn Gly Val Met Gln Met Gly Leu Ala Glu Asn Gln
45 50 55

ctt acc tct gat ttg gtt gaa g at tgg ata ctg aac aac cct gaa gcc 306
Leu Thr Ser Asp Leu Val Glu Asp Trp Ile Leu Asn Asn Pro Glu Ala
60 65 70

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<p>tcc att tgc act cca gaa gga ata aat gat ttc agg gcc ata gct aac Ser Ile Cys Thr Pro Glu Gly Ile Asn Asp Phe Arg Ala Ile Ala Asn 75 80 85</p>	<p>354</p>	
<p>ttt cag gat tat cat ggt ctg gcc gag ttc aga aat gct gtg gct aaa Phe Gln Asp Tyr His Gly Leu Ala Glu Phe Arg Asn Ala Val Ala 90 95 100 105</p>	<p>402</p>	<p>Lys</p>
<p>ttt atg gct aga aca agg gga aac aga atc acg ttt gac cct gac cgt Phe Met Ala Arg Thr Arg Gly Asn Arg Ile Thr Phe Asp Pro Asp Arg 110 115 120</p>	<p>450</p>	
<p>att gtc atg agc ggt gga gcc acc gga gca cac gaa gtc act gcc ttt Ile Val Met Ser Gly Gly Ala Thr Gly Ala His Glu Val Thr Ala Phe 125 130 135</p>	<p>498</p>	
<p>tgt ttg gca gat ccc ggc gag gca ttc tta gtg ccc att ccc tat tat Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Ile Pro Tyr Tyr 140 145 150</p>	<p>546</p>	
<p>cca ggc ttt gac cgg gat ttg agg tgg aga aca gga gtt aaa ctt gtt Pro Gly Phe Asp Arg Asp Leu Arg Trp Arg Thr Gly Val Lys Leu Val 155 160 165</p>	<p>594</p>	
<p>cca gtt atg tgc gat agc tca aat aat t tc gtg ttg aca aag gaa gca Pro Val Met Cys Asp Ser Ser Asn Asn Phe Val Leu Thr Lys Glu Ala 170 175 180 185</p>	<p>642</p>	
<p>ttg gaa gat gcc tat gag aaa gca aga gag gat aac atc aga gta aag Leu Glu Asp Ala Tyr Glu Lys Ala Arg Glu Asp Asn Ile Arg Val Lys 190 195 2</p>	<p>690</p>	<p>00</p>
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<p>aga aag aca ctg aga acc gtg gtg agc ttc atc aat gag aag cgt atc Arg Lys Thr Leu Arg Thr Val Val Ser Phe Ile Asn Glu Lys Arg Ile 220 225 230</p>	<p>786</p>	
<p>cac ctt gta tgt gat gaa ata tat gct gca aca gtt ttc agc caa ccc His Leu Val Cys Asp Glu Ile Tyr Ala Ala Thr Val Phe Ser Gln Pro 235 240 245</p>	<p>834</p>	
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Gly Phe Pro Gly Phe Arg Val Gly Ile Ile Tyr Ser Tyr Asn Asp Ala			
285	290	295	
gtg gtt aat tgt gca cgc aaa atg tca agc ttt gga ttg gtg tca aca	1026		
Val Val Asn Cys Ala Arg Lys Met Ser Ser Phe Gly Leu Val Ser Thr			
300	305	310	
cag act cag tat ctt tta gca tcg atg cta aat gat gat gag ttt gtg	1074		
Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Asn Asp Asp Glu Phe Val			
315	320	325	
gag agg ttt ctg gca gag agt gca aag agg ttg gct caa agg ttc agg	1122		
Glu Arg Phe Leu Ala Glu Ser Ala Lys Arg Leu Ala Gln Arg Phe Arg			
330	335	340	345
gtt ttc act g gg ggg ttg gcc aaa gtt ggc ata aag tgc ttg caa agc	1170		
Val Phe Thr Gly Gly Leu Ala Lys Val Gly Ile Lys Cys Leu Gln Ser			
350	355	360	
aat gct ggt cta ttt gtg tgg atg gat tta agg caa ctt ctc aaa aag	1218		
Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg Gln Leu Leu Lys Lys			
365	370	375	
cca act ttc gac tct gaa acg gag ctt tgg aaa gtt atc att cat gaa	1266		
Pro Thr Phe Asp Ser Glu Thr Glu Leu Trp Lys	Val Ile Ile His Glu		
380	385	390	
gtt aag atc aat gtt tca cct ggc tat tcc ttc cat tgc a	ct gag cca	1314	
Val Lys Ile Asn Val Ser Pro Gly Tyr Ser Phe His Cys Thr Glu Pro			
395	400	405	
ggg tgg ttt agg gtg tgc tat gcc aac atg gat gat atg gct gtg caa	1362		
Gly Trp Phe Arg Val Cys Tyr Ala Asn Met Asp Asp Met Ala Val Gln			
410	415	420	425
att gct ttg caa cga atc cgc aac ttt gtg ctt caa aac aag gag gtc	1410		
Ile Ala Leu Gln Arg Ile Arg Asn Phe Val Leu Gln Asn Lys Glu Val			
430	435	440	
gtg gtg tct aat aag aaa cat tgt tgg cac agt aac ttg agg ctg agc	1458		
Val Val Ser Asn Lys Lys His Cys Trp His Ser Asn Leu Arg Leu Ser			
445	450	455	
ctc aaa acc aga agg t tt gat gat atc acc atg tca cct cac tct ccc	1506		
Leu Lys Thr Arg Arg Phe Asp Asp Ile Thr Met Ser Pro His Ser Pro			
460	465	470	

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cta cct cag tca cct atg gtt aaa gcc aca aat tgagtttgca tattcctctg 1559
Leu Pro Gln Ser Pro Met Val Lys Ala Thr Asn
475                                480

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gtttatagag tctgtaatgt tattggttta tcagaagagt ccaaagatg tctgtaatct 1859

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SEQ ID NO:2

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Ile Gly Asp Gly His Gly Glu Ser Ser Pro Tyr Phe Asp Gly Trp Lys
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Ala Tyr Asp Gln Asn Pro Phe His Pro Thr Asp Asn Pro Asn Gly Val
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Met Gln Met Gly Leu Ala Glu Asn Gln Leu Thr Ser Asp Leu Val Glu
          50              55              60

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Asp Trp Ile Leu Asn Asn Pro Glu Ala Ser Ile Cys Thr Pro Glu Gly
          65              70              75              80

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Ile Asn Asp Phe Arg Ala Ile Ala Asn Phe Gln Asp Tyr His Gly Leu
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Ala Glu Phe Arg Asn Ala Val Ala Lys Phe Met Ala Arg Thr Arg Gly
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Asn Arg Ile T   hr Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala
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Thr Gly Ala His Glu Val      Thr Ala Phe Cys Leu Ala Asp Pro Gly Glu

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Arg Trp Arg Thr Gly Val Lys Leu Val Pro Val		Met Cys Asp Ser Ser	
	165	170	175
Asn Asn Phe Val Leu Thr Lys Glu Ala Leu Glu Asp Ala T			yr Glu Lys
	180	185	190
Ala Arg Glu Asp Asn Ile Arg Val Lys Gly Leu Leu Ile Thr Asn Pro			
	195	200	205
Ser Asn Pro Leu Gly Thr Ile Met Asp Arg Lys Thr Leu Arg Thr Val			
	210	215	220
Val Ser Phe Ile Asn Glu Lys Arg Ile His Leu Val Cys Asp Glu Ile			
	225	230	235
Tyr Ala Ala Thr Val Phe Ser Gln Pro Gly Phe Ile Ser Ile Ala Glu			
	245	250	255
Ile Leu Glu Asp Glu Thr Asp Ile Glu Cys Asp Arg Asn Leu Val His			
	260	265	270
Ile Val Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val			
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Gly Ile Ile Tyr Ser Tyr Asn Asp Ala Val Val Asn Cys Ala Arg Lys			300
	290	295	
Met Ser Ser Phe Gly Leu Val Ser Thr Gln Thr Gln Tyr Leu Leu Ala			
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Ser Met Leu Asn Asp Asp Glu Phe Val Glu Arg Phe Leu Ala Glu Ser			
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Ala Lys Arg Leu Ala Gln Arg Phe Arg Val Phe Thr Gly Gly Leu Ala			
	340	345	350
Lys Val Gly Ile Lys Cys Leu Gln Ser Asn Ala Gly Leu Phe Val Trp			
	355	360	365
Met Asp Leu Arg Gln Leu Leu Lys Lys Pro Thr Phe Asp Ser Glu Thr			
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Glu Leu Trp Lys Val Ile Ile His Glu Val Lys Ile Asn Val Ser Pro			
	385	390	395
			400

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Gly Tyr Ser Phe His Cys Thr Glu Pro Gly Trp Phe Arg Val Cys Tyr
405 410 415

Ala Asn Met Asp Asp Met Ala Val Gln Ile Ala Leu Gln Arg Ile Arg
420 425 430

Asn Phe Val Leu Gln Asn Lys Glu Val Val Val Ser Asn Lys Lys His
435 440 445

Cys Trp His Ser Asn Leu Arg Leu Ser Leu Lys Thr Arg Arg Phe Asp
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atgcatttta tctagaagct gggaactgaa ccaaaaaaat agccagttga acaactgcag 240

tatttgtagg cgtattcatt tctcctttcc tacaataatc cttggttgct ctttatcgga 300

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gcgtgctgtc gaagaacaca taattttgag gttgaagctc acgtgcgagt tttgcatatt 420

tttaggttat gtgtacacgt atggagttag ttccgcgtat atagttagg tagttgag tg 480

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aactccgggc ttttggtgag tacaactttt ctactcttat ttaatggagg gattatTTTT 660

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tatccaatgc attataaata cacactctcc ctcccttcta ttcttcattg cat cacattt 2340

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2nd Substitute Specification – Clean Version

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